

SEQUENCE LISTING

<110> Estell, David Aaron

<120> Human Protease and Use of Such Protease for Pharmaceutical Applications and for Reducing the Allergenicity of Non-Human Proteins

<130> GC532

<140> 09/060, 854

<141> 1998-04-15

<160> 6

170> EastSEO for Windows Version 3.0

<210> 1

<211> 1545

<212> DNA

<213> B. amyloliquefaciens

<220>

<221> CDS

<222> (96) . . . (416)

<221> mat_peptide

<222> (417) ... (1545)

<pre> <400> 1 ggtctactaa aatattattc catactatac aatataaca cagaataatc tgtctattgg ttattctgca aataaaaaaaa aggagaggat aaaga gtg aga ggc aaa aaa gta Val Arg Gly Lys Lys Val 1 5 </pre>	60 113
<pre> tgg atc agt ttg ctg ttt gct tta gcg tta atc ttt acg atg gcg ttc Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu Ile Phe Thr Met Ala Phe 10 15 20 </pre>	161
<pre> ggc agc aca tcc tct gcc cag gcg gca ggg aaa tca aac ggg gaa aag Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly Lys Ser Asn Gly Glu Lys 25 30 35 </pre>	209
<pre> aaa tat att gtc ggg ttt aaa cag aca atg agc acg atg agc gcc gct Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser Thr Met Ser Ala Ala 40 45 50 </pre>	257
<pre> aag aag aaa gat gtc att tct gaa aaa ggc ggg aaa gtg caa aag caa Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Lys Val Gln Lys Gln 55 60 65 </pre>	305
<pre> ttc aaa tat gta gac gca gct tca gtc aca tta aac gaa aaa gct gta Phe Lys Tyr Val Asp Ala Ala Ser Val Thr Leu Asn Glu Lys Ala Val 75 80 85 </pre>	353
<pre> aaa gaa ttg aaa aaa gac ccg agc gtc gct tac gtt gaa gaa gat cac Lys Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His </pre>	401

90

95

100

gta gca cat gcg tac ggcgcgtccg tgccttacgg cgtatcacaa attaaagccc	456
Val Ala His Ala Tyr	
105	

ctgctctgca ctctcaaggc tacactggat caaatgttaa agtagcggtt atcgacagcg	516
gtatcgattc ttctcatcct gatttaaagg tagcaagcgg agccagcatg gttccttctg	576
aaacaaatcc tttccaagac aacaactctc acggaactca cggtgccggc acagttcgg	636
ctcttaataa ctcaatcggt gtattaggcg ttgcgccaag cgcacactt tacgctgtaa	696
aagttctcg tgctgacggg tccggccaaat acagctggat cattaacggg atcgagtggg	756
cgatcgcaaa caatatggac gttattaaca tgagcctcg ggaccccttct ggttctgctg	816
ctttaaaagc ggcagttgat aaagccgttg catccggcgt cgtagtcgtt gccgcagccg	876
gtaacgaagg cactccggc agctcaagca cagtgggcta ccctggtaaa tacccttctg	936
tcattgcagt aggccgtgtt gacagcagca accaaagagc atctttctca agcgtaggac	996
ctgagctga tgtcatggca cctggcgtat ctatccaaag cacgcttcct ggaaacaaat	1056
acggggcgtt caacgggtacg tcaatggcat ctccgcacgt tgccggagcg gctgcttga	1116
ttctttctaa gcacccgaac tggacaaaca ctcaagtccg cagcagttt gaaaacacca	1176
ctacaaaact tggtagttct ttgtactatg gaaaagggtt gatcaacgtt caagccggcag	1236
ctcagtaaaa cataaaaaac cggccttggaa tcaacgtaca agccggcagct cagtaaaaaca	1296
taaaaaaaaaccg gcctggcccc cggcgtttt ttattatttt tcttcctccg catgttcaat	1356
ccgctccata atcgacggat ggctccctct gaaaattttt acgagaaaacg gcgggttgac	1416
ccggctcagt cccgtaacgg ccaactccctg aaacgtctca atcgccgctt cccgggttcc	1476
ggtagctca atgcataac ggtcggcggc gtttccctga taccgggaga cggcattcgt	1536
aatcgatc	1545

<210> 2

<211> 275

<212> PRT

<213> B. amyloliquefaciens

<400> 2

Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu	
1 5 10 15	
His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp	
20 25 30	
Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala	
35 40 45	
Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His	
50 55 60	
Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly	
65 70 75 80	
Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu	
85 90 95	
Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu	
100 105 110	
Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly	
115 120 125	
Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala	
130 135 140	
Ser Gly Val Val Val Val Ala Ala Gly Asn Glu Gly Thr Ser Gly	
145 150 155 160	
Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala	
165 170 175	
Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val	
180 185 190	
Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr	

195	200	205
Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser		
210	215	220
Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn		
225	230	235
Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Lys		240
245	250	255
Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala		
260	265	270
Ala Ala Gln		
275		

<210> 3
<211> 269
<212> PRT
<213> B. lenticus

195	200	205
Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser		
210	215	220
Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn		
225	230	235
Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Lys		240
245	250	255
Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala		
260	265	270
Ala Ala Gln		
275		
<400> 3		
Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala		
1	5	10
His Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp		
20	25	30
Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser		
35	40	45
Phe Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr		
50	55	60
His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu		
65	70	75
Gly Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala		
85	90	95
Ser Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala		
100	105	110
Gly Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser		
115	120	125
Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly		
130	135	140
Val Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser		
145	150	155
Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln		
165	170	175
Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile		
180	185	190
Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr		
195	200	205
Ala Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ala		
210	215	220
Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile		
225	230	235
Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu		
245	250	255
Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg		
260	265	

<210> 4
<211> 274
<212> PRT
<213> B. licheniformis

<400> 4
 Ala Gln Thr Val Pro Tyr Gly Ile Pro Leu Ile Lys Ala Asp Lys Val
 1 5 10 15
 Gln Ala Gln Gly Phe Lys Gly Ala Asn Val Lys Val Ala Val Leu Asp
 20 25 30
 Thr Gly Ile Gln Ala Ser His Pro Asp Leu Asn Val Val Gly Gly Ala
 35 40 45
 Ser Phe Val Ala Gly Glu Ala Tyr Asn Thr Asp Gly Asn Gly His Gly
 50 55 60
 Thr His Val Ala Gly Thr Val Ala Ala Leu Asp Asn Thr Thr Gly Val
 65 70 75 80
 Leu Gly Val Ala Pro Ser Val Ser Leu Tyr Ala Val Lys Val Leu Asn
 85 90 95
 Ser Ser Gly Ser Gly Ser Tyr Ser Gly Ile Val Ser Gly Ile Glu Trp
 100 105 110
 Ala Thr Thr Asn Gly Met Asp Val Ile Asn Met Ser Leu Gly Gly Ala
 115 120 125
 Ser Gly Ser Thr Ala Met Lys Gln Ala Val Asp Asn Ala Tyr Ala Arg
 130 135 140
 Gly Val Val Val Val Ala Ala Ala Gly Asn Ser Gly Asn Ser Gly Ser
 145 150 155 160
 Thr Asn Thr Ile Gly Tyr Pro Ala Lys Tyr Asp Ser Val Ile Ala Val
 165 170 175
 Gly Ala Val Asp Ser Asn Ser Asn Arg Ala Ser Phe Ser Ser Val Gly
 180 185 190
 Ala Glu Leu Glu Val Met Ala Pro Gly Ala Gly Val Tyr Ser Thr Tyr
 195 200 205
 Pro Thr Asn Thr Tyr Ala Thr Leu Asn Gly Thr Ser Met Ala Ser Pro
 210 215 220
 His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn Leu
 225 230 235 240
 Ser Ala Ser Gln Val Arg Asn Arg Leu Ser Ser Thr Ala Thr Tyr Leu
 245 250 255
 Gly Ser Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Glu Ala Ala
 260 265 270
 Ala Gln

Asp Ser Thr Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
 100 105 110
 Trp Ala Ile Ser Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
 115 120 125
 Pro Thr Gly Ser Thr Ala Leu Lys Thr Val Val Asp Lys Ala Val Ser
 130 135 140
 Ser Gly Ile Val Val Ala Ala Ala Gly Asn Glu Gly Ser Ser Gly
 145 150 155 160
 Ser Thr Ser Thr Val Gly Tyr Pro Ala Lys Tyr Pro Ser Thr Ile Ala
 165 170 175
 Val Gly Ala Val Asn Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Ala
 180 185 190
 Gly Ser Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
 195 200 205
 Leu Pro Gly Gly Thr Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Thr
 210 215 220
 Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Thr
 225 230 235 240
 Trp Thr Asn Ala Gln Val Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr
 245 250 255
 Leu Gly Asn Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
 260 265 270
 Ala Ala Gln
 275

<210> 6
 <211> 1052
 <212> PRT
 <213> Human subtilisin

<400> 6
 Met Lys Leu Val Asn Ile Trp Leu Leu Leu Val Val Leu Leu Cys
 1 5 10 15
 Gly Lys Lys His Leu Gly Asp Arg Leu Glu Lys Lys Ser Phe Glu Lys
 20 25 30
 Ala Pro Cys Pro Gly Cys Ser His Leu Thr Leu Lys Val Glu Phe Ser
 35 40 45
 Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe Asn Gly Tyr Phe
 50 55 60
 Thr Ala Lys Ala Arg Asn Ser Phe Ile Ser Ser Ala Leu Lys Ser Ser
 65 70 75 80
 Glu Val Asp Asn Trp Arg Ile Ile Pro Arg Asn Asn Pro Ser Ser Asp
 85 90 95
 Tyr Pro Ser Asp Phe Glu Val Ile Gln Ile Lys Glu Lys Gln Lys Ala
 100 105 110
 Gly Leu Leu Thr Leu Glu Asp His Pro Asn Ile Lys Arg Val Thr Pro
 115 120 125
 Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp Pro Thr
 130 135 140
 Val Pro Cys Asn Glu Thr Arg Trp Ser Gln Lys Trp Gln Ser Ser Arg
 145 150 155 160
 Pro Leu Arg Arg Ala Ser Leu Ser Leu Gly Ser Gly Phe Trp His Ala
 165 170 175
 Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln
 180 185 190
 Val Ala Gln Thr Leu Gln Ala Asp Val Leu Trp Gln Met Gly Tyr Thr
 195 200 205

Gly Ala Asn Val Arg Val Ala Val Phe Asp Thr Gly Leu Ser Glu Lys
 210 215 220
 His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn Trp Thr Asn Glu
 225 230 235 240
 Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe Val Ala Gly Val
 245 250 255
 Ile Ala Ser Met Arg Glu Cys Gln Gly Phe Ala Pro Asp Ala Glu Leu
 260 265 270
 His Ile Phe Arg Val Phe Thr Asn Asn Gln Val Ser Tyr Thr Ser Trp
 275 280 285
 Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys Ile Asp Val Leu
 290 295 300
 Asn Leu Ser Ile Gly Gly Pro Asp Phe Met Asp His Pro Phe Val Asp
 305 310 315 320
 Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met Val Ser Ala Ile
 325 330 335
 Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn Pro Ala Asp Gln
 340 345 350
 Met Asp Val Ile Gly Val Gly Ile Asp Phe Glu Asp Asn Ile Ala
 355 360 365
 Arg Phe Ser Ser Arg Gly Met Thr Thr Trp Glu Leu Pro Gly Gly Tyr
 370 375 380
 Gly Arg Met Lys Pro Asp Ile Val Thr Tyr Gly Ala Gly Val Arg Gly
 385 390 395 400
 Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly Thr Ser Val Ala
 405 410 415
 Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val Ser Thr Val Gln
 420 425 430
 Lys Arg Glu Leu Val Asn Pro Ala Ser Met Lys Gln Ala Leu Ile Ala
 435 440 445
 Ser Ala Arg Arg Leu Pro Gly Val Asn Met Phe Glu Gln Gly His Gly
 450 455 460
 Lys Leu Asp Leu Leu Arg Ala Tyr Gln Ile Leu Asn Ser Tyr Lys Pro
 465 470 475 480
 Gln Ala Ser Leu Ser Pro Ser Tyr Ile Asp Leu Thr Glu Cys Pro Tyr
 485 490 495
 Met Trp Pro Tyr Cys Ser Gln Pro Ile Tyr Tyr Gly Gly Met Pro Thr
 500 505 510
 Val Val Asn Val Thr Ile Leu Asn Gly Met Gly Val Thr Gly Arg Ile
 515 520 525
 Val Asp Lys Pro Asp Trp Gln Pro Tyr Leu Pro Gln Asn Gly Asp Asn
 530 535 540
 Ile Glu Val Ala Phe Ser Tyr Ser Ser Val Leu Trp Pro Trp Ser Gly
 545 550 555 560
 Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala Ala Ser Trp Glu
 565 570 575
 Gly Ile Ala Gln Gly His Val Met Ile Thr Val Ala Ser Pro Ala Glu
 580 585 590
 Thr Glu Ser Lys Asn Gly Ala Glu Gln Thr Ser Thr Val Lys Leu Pro
 595 600 605
 Ile Lys Val Lys Ile Ile Pro Thr Pro Pro Arg Ser Lys Arg Val Leu
 610 615 620
 Trp Asp Gln Tyr His Asn Leu Arg Tyr Pro Pro Gly Tyr Phe Pro Arg
 625 630 635 640
 Asp Asn Leu Arg Met Lys Asn Asp Pro Leu Asp Trp Asn Gly Asp His
 645 650 655
 Ile His Thr Asn Phe Arg Asp Met Tyr Gln His Leu Arg Ser Met Gly

	660	665	670												
Tyr	Phe	Val	Glu	Val	Leu	Gly	Ala	Pro	Phe	Thr	Cys	Phe	Asp	Ala	Ser
	675			680							685				
Gln	Tyr	Gly	Thr	Leu	Leu	Met	Val	Asp	Ser	Glu	Glu	Glu	Tyr	Phe	Pro
	690			695						700					
Glu	Glu	Ile	Ala	Lys	Leu	Arg	Arg	Asp	Val	Asp	Asn	Gly	Leu	Ser	Leu
	705			710					715				720		
Val	Ile	Phe	Ser	Asp	Trp	Tyr	Asn	Thr	Ser	Val	Met	Arg	Lys	Val	Lys
	725					730						735			
Phe	Tyr	Asp	Glu	Asn	Thr	Arg	Gln	Trp	Trp	Met	Pro	Asp	Thr	Gly	Gly
						740			745			750			
Ala	Asn	Ile	Pro	Ala	Leu	Asn	Glu	Leu	Leu	Ser	Val	Trp	Asn	Met	Gly
						755			760			765			
Phe	Ser	Asp	Gly	Leu	Tyr	Glu	Gly	Glu	Phe	Thr	Leu	Ala	Asn	His	Asp
						770			775			780			
Met	Tyr	Tyr	Ala	Ser	Gly	Cys	Ser	Ile	Ala	Lys	Phe	Pro	Glu	Asp	Gly
						785			790			795			800
Val	Val	Ile	Thr	Gln	Thr	Phe	Lys	Asp	Gln	Gly	Leu	Glu	Val	Leu	Lys
						805			810			815			
Gln	Glu	Thr	Ala	Val	Val	Glu	Asn	Val	Pro	Ile	Leu	Gly	Leu	Tyr	Gln
						820			825			830			
Ile	Pro	Ala	Glu	Gly	Gly	Arg	Ile	Val	Leu	Tyr	Gly	Asp	Ser	Asn	
						835			840			845			
Cys	Leu	Asp	Asp	Ser	His	Arg	Gln	Lys	Asp	Cys	Phe	Trp	Leu	Leu	Asp
						850			855			860			
Ala	Leu	Leu	Gln	Tyr	Thr	Ser	Tyr	Gly	Val	Thr	Pro	Pro	Ser	Leu	Ser
						865			870			875			880
His	Ser	Gly	Asn	Arg	Gln	Arg	Pro	Pro	Ser	Gly	Ala	Gly	Ser	Val	Thr
						885			890			895			
Pro	Glu	Arg	Met	Glu	Gly	Asn	His	Leu	His	Arg	Tyr	Ser	Lys	Val	Leu
						900			905			910			
Glu	Ala	His	Leu	Gly	Asp	Pro	Lys	Pro	Arg	Pro	Leu	Pro	Ala	Cys	Pro
						915			920			925			
Arg	Leu	Ser	Trp	Ala	Lys	Pro	Gln	Pro	Leu	Asn	Glu	Thr	Ala	Pro	Ser
						930			935			940			
Asn	Leu	Trp	Lys	His	Gln	Lys	Leu	Leu	Ser	Ile	Asp	Leu	Asp	Lys	Val
						945			950			955			960
Val	Leu	Pro	Asn	Phe	Arg	Ser	Asn	Arg	Pro	Gln	Val	Arg	Pro	Leu	Ser
						965			970			975			
Pro	Gly	Glu	Ser	Gly	Ala	Trp	Asp	Ile	Pro	Gly	Gly	Ile	Met	Pro	Gly
						980			985			990			
Arg	Tyr	Asn	Gln	Glu	Val	Gly	Gln	Thr	Ile	Pro	Val	Phe	Ala	Phe	Leu
						995			1000			1005			
Gly	Ala	Met	Val	Val	Leu	Ala	Phe	Phe	Val	Val	Gln	Ile	Asn	Lys	Ala
						1010			1015			1020			
Lys	Ser	Arg	Pro	Lys	Arg	Arg	Lys	Pro	Arg	Val	Lys	Arg	Pro	Gln	Leu
						1025			1030			1035			104
Met	Gln	Gln	Val	His	Pro	Pro	Lys	Thr	Pro	Ser	Val				
						1045			1050						